Molecular tracing of aquatic viruses - MOLTRAQ

Mikkelsen, Susie Sommer; Schuetze, H.; Korsholm, H.; Jensen, B. Bang; Olesen, Niels Jørgen

Publication date:
2014

Document Version
Early version, also known as pre-print

MOLECULAR TRACING OF AQUATIC VIRUSES - MOLTRAQ

Mikkelsen S. S.[1], Schuetze H.[2], Korsholm H.[3], Bruun M. S.[1], Olesen N.J.[1]

susmi@dtu.vet.dk [1]DTU Vet National Veterinary Institute, Bülowsvej 27 1870 Frederiksberg C,

[2]Friedrich-Loeffler Institut, Insel Riems, Germany

Danish Veterinary and Food Administration, Tysklandsvej 7, 7100 Vejle [3]

Abstract:

MOLTRAQ is a pan-European project that aims to increase knowledge on a wide array of economically important viral diseases in fish and molluscs on both the epidemiological and the genetic level. Spatio-temporal and phylogenetic information will be used to create phylogeographic and scenario-simulation models to identify important factors for the spread of disease and control strategies.

Viral haemorrhagic septicaemia Virus (VHSV) is one of the most important viral fish diseases and is widely spread all over Europe and creates significant losses every year for European fish farmers. VHSV has been endemic in Denmark since the 1950's but after an effective control and eradication programme that spanned more than 45 years the virus was finally eradicated from Denmark in 2009.

As the OIE and EU reference laboratory for VHSV, the Danish national reference laboratory for fish diseases has a large collection of Danish VHSV isolates that span over more than 50 years. As part of MOLTRAQ more than 200 Danish isolates spanning from 1978-2003 has been sequenced and epidemiological information has been collected.

This information will form the basis for several different areas of research in the MOLTRAQ project. Data will be used to create a spatio-temporal computermodel for VHS in Denmark that will be able to provide information about control strategies in countries or areas with a similar spread of disease history. This work will be done in close collaboration with the National Veterinary institute in Norway and the Norwegian Computing Center.

Data will also be used to create phylogenetic and phylogeographic models to help infer the relationship between VHS outbreaks in Denmark and to look into the spread of the disease over a historical period. Some of these data will be presented at the Annual Workshop.

Furthermore, data will be used to create phylogenetic and phylogeographic models at a wider European scale.

MOLTRAQ is funded under the EMIDA-ERA Net under the EU 7th Framework program (For more details about EMIDA: www.emida-era.net).

Partners into the project are: Norwegian Veterinary Institute (NO, Coordinator), Technical University of Denmark-National Veterinary Institute (DK), Agence Nationale de Sécurité Sanitaire (FR), Friedrich-Loeffler Institut (DE), Institut Francais de Recherche pour l'Exploitation de la Mer (FR), Institut de Recherche pour le Développement (FR) and Norwegian Computing Center (NO).